

RL Gene 234:71-79(1999).
 DR EMBL: AB019623; BAA7351.1; -
 DR InterPro: IPR001296; Glycosyl_transf.1.
 DR InterPro: IPR000794; Ketocacyl-synt.
 DR Pfam: PF00534; Glycosyl_transf.1; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR Glycosyltransferase; Transferase.
 KW SEQUENCE 605 AA; 66345 MW; 60A81627678722B CRC64;

Query Match 62.8%; Score 2037.5; DB 10; Length 605;
 Best Local Similarity 63.7%; Pred. No. 1.6e-148;
 Matches 381; Conservative 85; Mismatches 113; Indels 19; Gaps 6;

28 GLAFQIRIPYLSNASTFEGLRSN---OMNSRPMQCAKATTRQYKGIQHASRRPSV 83
 17 GTDRFR-----AGFGVRRSPADAPLGMRTTGASAPRQSKAKHRCRCLSM 68
 84 IC-----ASGMNLIYAALVAPMSTGTGLGVLGGLPPMAAKGHRVMTIARHDOYKDW 139
 69 VVRATGSGMNLVFGAEMAPMSTGTGLGVLGGLPPMAANGHRVMTISPRYDOYKDW 128
 140 DTAFFVELKVDRIETVRFPHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 129
 129 DTSVSEIKVADEYERVRYFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 188
 200 NQRLFCCLATLETPRVLPNNKRYHSGPKGED-LFIANDMHTALPCYKTYVQAAG 258
 189 NQRLFCCLATLETPRVLPNNKRYHSGPKGED-LFIANDMHTALPCYKTYVQAAG 258
 259 IYKAKAVAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPKIKRINMMAKI 318
 248 IYKAKAVAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPKIKRINMMAKI 307
 319 IESDRALVSPYAAQELVSGIDKGVLELDNLLRLKTCIGIINGMDTNMNPSTKYITANY 378
 308 LQAKKVLTVSPYAAQELVSGIDKGVLELDNLLRLKTCIGIINGMDTNMNPSTKYITANY 367
 379 DATVMEKPLNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DODVQ 437
 368 DVTALBEKALNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DODVQ 427
 438 VIVGTGKKKLEROLALDEFPDKFRAHMKFNIPLAHGIAGADIVIPSRFPCGLIQ 497
 428 IVLTGKKKLEROLALDEFPDKFRAHMKFNIPLAHGIAGADIVIPSRFPCGLIQ 487
 498 LOGMRVGTGPGACASTGGLVDTIMEGKTFHMGRLSDVCNVEPADVKKVYTTIKRAVKY 547
 558 GTPAFEEIOMNCAODPSKGPRAKEMKFLSLGLESGEAGIEEVEVAPLAKENAVAP 615
 548 GTPAFEEIOMNCAODPSKGPRAKEMKFLSLGLESGEAGIEEVEVAPLAKENAVAP 605

RESULT 14

09F006 PRELIMINARY; PRT; 605 AA.

ID 09F006
 AC 09F006
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Granule bound starch synthase 1 (EC 2.4.1.21).
 GN GBSST.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. CHEYENNE; TISSUE-ENDOSPERM;
 RA McCue K.E., Hurkman W.J., Tanaka C.K., Anderson O.D.;
 ST Starch Branching Enzymes SpeI and Sbe2 from Wheat (Triticum aestivum

RT cv. Cheyenne); Molecular Characterization, Developmental Expression,
 RT and Homolog Assignment by Differential PCR.
 RL Submitted (Jun-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF263320; AAC27624.1; -
 DR InterPro: IPR001296; Glycosyl_transf.1.
 DR InterPro: IPR000794; Ketocacyl-synt.
 DR Pfam: PF00534; Glycosyl_transf.1; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR Glycosyltransferase; Transferase.
 KW SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

Query Match 62.8%; Score 2037.5; DB 10; Length 605;
 Best Local Similarity 63.7%; Pred. No. 1.6e-148;
 Matches 381; Conservative 85; Mismatches 113; Indels 19; Gaps 6;

28 GLAFQIRIPYLSNASTFEGLRSN---OMNSRPMQCAKATTRQYKGIQHASRRPSV 83
 17 GTDRFR-----AGFGVRRSPADAPLGMRTTGASAPRQSKAKHRCRCLSM 68
 84 IC-----ASGMNLIYAALVAPMSTGTGLGVLGGLPPMAAKGHRVMTIARHDOYKDW 139
 69 VVRATGSGMNLVFGAEMAPMSTGTGLGVLGGLPPMAANGHRVMTISPRYDOYKDW 128
 140 DTAFFVELKVDRIETVRFPHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 129
 129 DTSVSEIKVADEYERVRYFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 188
 200 NQRLFCCLATLETPRVLPNNKRYHSGPKGED-LFIANDMHTALPCYKTYVQAAG 258
 189 NQRLFCCLATLETPRVLPNNKRYHSGPKGED-LFIANDMHTALPCYKTYVQAAG 258
 259 IYKAKAVAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPKIKRINMMAKI 318
 248 IYKAKAVAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPKIKRINMMAKI 307
 319 IESDRALVSPYAAQELVSGIDKGVLELDNLLRLKTCIGIINGMDTNMNPSTKYITANY 378
 308 LQAKKVLTVSPYAAQELVSGIDKGVLELDNLLRLKTCIGIINGMDTNMNPSTKYITANY 367
 379 DATVMEKPLNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DODVQ 437
 368 DVTALBEKALNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DODVQ 427
 438 VIVGTGKKKLEROLALDEFPDKFRAHMKFNIPLAHGIAGADIVIPSRFPCGLIQ 497
 428 IVLTGKKKLEROLALDEFPDKFRAHMKFNIPLAHGIAGADIVIPSRFPCGLIQ 487
 498 LOGMRVGTGPGACASTGGLVDTIMEGKTFHMGRLSDVCNVEPADVKKVYTTIKRAVKY 547
 558 GTPAFEEIOMNCAODPSKGPRAKEMKFLSLGLESGEAGIEEVEVAPLAKENAVAP 615
 548 GTPAFEEIOMNCAODPSKGPRAKEMKFLSLGLESGEAGIEEVEVAPLAKENAVAP 605

RESULT 15

09SL56 PRELIMINARY; PRT; 604 AA.

ID 09SL56
 AC 09SL56
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Starch synthase (GBSSI) (EC 2.4.1.21).
 GN MAY.
 OS Triticum turgidum subsp. durum (durum wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OC NCBI_TaxID=4567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Murali J., Talra T., Ohta D.;